

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Bandman, Olga
 Hillman, Jennifer L.
 Corley, Neil C.
 Guegler, Karl G.
 Lal, Preeti
 Goli, Surya K.
 Shah, Purvi

(ii) TITLE OF THE INVENTION: DISEASE ASSOCIATED PROTEIN KINASES

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 (B) STREET: 3174 Porter Drive
 (C) CITY: Palo Alto
 (D) STATE: CA
 (E) COUNTRY: USA
 (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
 (B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
 (B) REGISTRATION NUMBER: 36,749
 (C) REFERENCE/DOCKET NUMBER: PF-0321 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555
 (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 685 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HUVENOB01
 (B) CLONE: 39043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Glu	Leu	Leu	Arg	Thr	Ile	Thr	Tyr	Gln	Pro	Ala	Ala	Ser	Thr	Lys
1				5					10					15	
Met	Cys	Glu	Gln	Ala	Leu	Gly	Lys	Gly	Cys	Gly	Ala	Asp	Ser	Lys	Lys
			20					25					30		
Lys	Arg	Pro	Pro	Gln	Pro	Pro	Glu	Glu	Ser	Gln	Pro	Pro	Gln	Ser	Gln


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Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
      435      440      445
Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
      450      455      460
Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
465      470      475      480
Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
      485      490      495
Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
      500      505      510
Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
      515      520      525
Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Ala
      530      535      540
His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
545      550      555      560
Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
      565      570      575
His Tyr Met Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
      580      585      590
Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
      595      600      605
Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
      610      615      620
Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
625      630      635      640
Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
      645      650      655
Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
      660      665      670
Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
      675      680      685

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TBLYNOT01
- (B) CLONE: 40194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Pro Pro Lys Arg Asn Glu Lys Tyr Lys Leu Pro Ile Pro Phe Pro
 1      5      10      15
Glu Gly Lys Val Leu Asp Asp Met Glu Gly Asn Gln Trp Val Leu Gly
      20      25      30
Lys Lys Ile Gly Ser Gly Gly Phe Gly Leu Ile Tyr Leu Ala Phe Pro
      35      40      45
Thr Asn Lys Pro Glu Lys Asp Ala Arg His Val Val Lys Val Glu Tyr
      50      55      60
Gln Glu Asn Gly Pro Leu Phe Ser Glu Leu Lys Phe Tyr Gln Arg Val
65      70      75      80
Ala Lys Lys Asp Cys Ile Lys Lys Trp Ile Glu Arg Lys Gln Leu Asp
      85      90      95
Tyr Leu Gly Ile Pro Leu Phe Tyr Gly Ser Gly Leu Thr Glu Phe Lys
      100      105      110
Gly Arg Ser Tyr Arg Phe Met Val Met Glu Arg Leu Gly Ile Asp Leu
      115      120      125
Gln Lys Ile Ser Gly Gln Asn Gly Thr Phe Lys Lys Ser Thr Val Leu
      130      135      140

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Gln Leu Gly Ile Arg Met Leu Asp Val Leu Glu Tyr Ile His Glu Asn
145                      150                      155                      160

Glu Tyr Val His Gly Asp Val Lys Ala Ala Asn Leu Leu Leu Gly Tyr
                      165                      170                      175
Lys Asn Pro Asp Gln Val Tyr Leu Ala Asp Tyr Gly Leu Ser Tyr Arg
                      180                      185                      190
Tyr Cys Pro Asn Gly Asn His Lys Gln Tyr Gln Glu Asn Pro Arg Lys
                      195                      200                      205
Gly His Asn Gly Thr Ile Glu Phe Thr Ser Leu Asp Ala His Lys Gly
                      210                      215                      220
Val Gly Glu Ile Ala Gln Phe Leu Val Cys Ala His Ser Leu Ala Tyr
225                      230                      235                      240
Asp Glu Lys Pro Asn Tyr Gln Ala Leu Lys Lys Ile Leu Asn Pro His
                      245                      250                      255
Gly Ile Pro Leu Gly Pro Leu Asp Phe Ser Thr Lys Gly Gln Ser Ile
                      260                      265                      270
Asn Val His Thr Pro Asn Ser Gln Lys Val Asp Ser Gln Lys Ala Ala
                      275                      280                      285
Thr Lys Gln Val Asn Lys Ala His Asn Arg Leu Ile Glu Lys Lys Val
290                      295                      300
His Ser Glu Arg Ser Ala Glu Ser Cys Ala Thr Trp Lys Val Gln Lys
305                      310                      315                      320
Glu Glu Lys Leu Ile Gly Leu Met Asn Asn Glu Ala Ala Gln Glu Ser
                      325                      330                      335
Thr Arg Arg Arg Gln Lys Tyr Gln Glu Ser Gln Glu Pro Leu Asn Glu
                      340                      345                      350
Val Asn Ser Phe Pro Gln Lys Ile Ser Tyr Thr Gln Phe Pro Asn Ser
                      355                      360                      365
Phe Tyr Glu Pro His Gln Asp Phe Thr Ser Pro Asp Ile Phe Lys Lys
370                      375                      380
Ser Arg Ser Pro Ser Trp Tyr Lys Tyr Thr Ser Thr Val Ser Thr Gly
385                      390                      395                      400
Ile Thr Asp Leu Glu Ser Ser Thr Gly Leu Trp Pro Thr Ile Ser Gln
                      405                      410                      415
Phe Thr Leu Ser Glu Glu Thr Asn Ala Asp Val Tyr Tyr Tyr Arg Ile
                      420                      425                      430
Ile Ile Pro Val Leu Leu Met Leu Val Phe Leu Ala Leu Phe Phe Leu
435                      440                      445

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TMLR3DT01
- (B) CLONE: 402339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro
1                      5                      10                      15
Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala
                      20                      25                      30
Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
                      35                      40                      45
Gln Gln Lys Lys Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val
50                      55                      60
Gly Glu Leu Lys Asp Asp Asp Phe Glu Arg Ile Ser Glu Leu Gly Ala
65                      70                      75                      80
Gly Asn Gly Gly Val Val Thr Lys Val Gln His Arg Pro Ser Gly Leu
                      85                      90                      95

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Ile Met Ala Arg Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg
      100      105      110
Asn Gln Ile Ile Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro
      115      120      125
Tyr Ile Val Gly Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser
      130      135      140
Ile Cys Met Glu His Met Asp Gly Gly Ser Leu Asp His Leu Leu Lys
      145      150      155      160
Glu Ala Lys Arg Ile Pro Glu Glu Ile Leu Gly Lys Val Ser Ile Ala
      165      170      175
Val Leu Arg Gly Leu Ala Tyr Leu Arg Glu Lys His Gln Ile Met His
      180      185      190
Arg Asp Val Lys Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile
      195      200      205
Lys Leu Cys Asp Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala
      210      215      220
Asn Ser Phe Val Gly Thr Arg Ser Tyr Met Ala Pro Glu Arg Leu Gln
      225      230      235      240
Gly Thr His Tyr Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser
      245      250      255
Leu Val Glu Leu Ala Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala
      260      265      270
Lys Glu Leu Glu Ala Ile Phe Gly Arg Pro Val Val Asp Gly Glu Glu
      275      280      285
Gly Glu Pro His Ser Ile Ser Pro Arg Pro Arg Pro Gly Arg Pro
      290      295      300
Val Ser Gly His Gly Met Asp Ser Arg Pro Ala Met Ala Ile Phe Glu
      305      310      315      320
Leu Leu Asp Tyr Ile Val Asn Glu Pro Pro Pro Lys Leu Pro Asn Gly
      325      330      335
Val Phe Thr Pro Asp Phe Gln Glu Phe Val Asn Lys Cys Leu Ile Lys
      340      345      350
Asn Pro Ala Glu Arg Ala Asp Leu Lys Met Leu Thr Asn His Thr Phe
      355      360      365
Ile Lys Arg Ser Glu Val Glu Glu Val Asp Phe Ala Gly Trp Leu Cys
      370      375      380
Lys Thr Leu Arg Leu Asn Gln Pro Gly Thr Pro Thr Arg Thr Ala Val
      385      390      395      400

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT04
- (B) CLONE: 705365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Ala Met Thr Ala Gly Thr Thr Thr Thr Phe Pro Met Ser Asn His
1      5      10
Thr Arg Glu Arg Val Thr Val Ala Lys Leu Thr Leu Glu Asn Phe Tyr
      20      25      30
Ser Asn Leu Ile Leu Gln His Glu Glu Arg Glu Thr Arg Gln Lys Lys
      35      40      45
Leu Glu Val Ala Met Glu Glu Glu Gly Leu Ala Asp Glu Glu Lys Lys
      50      55      60
Leu Arg Arg Ser Gln His Ala Arg Lys Glu Thr Glu Phe Leu Arg Leu
      65      70      75      80
Lys Arg Thr Arg Leu Gly Leu Asp Asp Phe Glu Ser Leu Lys Val Ile
      85      90      95
Gly Arg Gly Ala Phe Gly Glu Val Arg Leu Val His Lys Lys Asp Thr

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			100					105					110				
Gly	His	Ile	Tyr	Ala	Met	Lys	Ile	Leu	Arg	Lys	Ser	Asp	Met	Leu	Glu		
		115						120				125					
Lys	Glu	Gln	Val	Ala	His	Ile	Arg	Ala	Glu	Arg	Asp	Ile	Leu	Val	Glu		
	130					135					140						
Ala	Asp	Gly	Ala	Trp	Val	Val	Lys	Met	Phe	Tyr	Ser	Phe	Gln	Asp	Lys		
145					150					155					160		
Arg	Asn	Leu	Tyr	Leu	Ile	Met	Glu	Phe	Leu	Pro	Gly	Gly	Asp	Met	Met		
			165					170						175			
Thr	Leu	Leu	Met	Lys	Lys	Asp	Thr	Leu	Thr	Glu	Glu	Glu	Thr	Gln	Phe		
		180						185					190				
Tyr	Ile	Ser	Glu	Thr	Val	Leu	Ala	Ile	Asp	Ala	Ile	His	Gln	Leu	Gly		
		195						200				205					
Phe	Ile	His	Arg	Asp	Ile	Lys	Pro	Asp	Asn	Leu	Leu	Leu	Asp	Ala	Lys		
	210					215					220						
Gly	His	Val	Lys	Leu	Ser	Asp	Phe	Gly	Ser	Cys	Thr	Gly	Leu	Lys	Lys		
225					230					235					240		
Ala	His	Arg	Thr	Glu	Phe	Tyr	Arg	Asn	Leu	Thr	His	Asn	Pro	Pro	Ser		
			245					250					255				
Asp	Phe	Ser	Phe	Gln	Asn	Met	Asn	Ser	Lys	Arg	Lys	Ala	Glu	Thr	Trp		
			260					265					270				
Lys	Lys	Asn	Arg	Arg	Gln	Leu	Ala	Tyr	Ser	Thr	Val	Gly	Thr	Pro	Asp		
		275					280					285					
Tyr	Ile	Ala	Pro	Glu	Val	Phe	Met	Gln	Thr	Gly	Tyr	Asn	Lys	Leu	Cys		
	290					295				300							
Asp	Trp	Trp	Ser	Leu	Gly	Val	Ile	Met	Tyr	Glu	Met	Leu	Ile	Gly	Tyr		
305					310					315					320		
Pro	Pro	Phe	Cys	Ser	Glu	Thr	Pro	Gln	Glu	Thr	Tyr	Arg	Lys	Val	Met		
			325					330						335			
Asn	Trp	Lys	Glu	Thr	Leu	Val	Phe	Pro	Pro	Glu	Val	Pro	Ile	Ser	Glu		
			340					345					350				
Lys	Ala	Lys	Asp	Leu	Ile	Leu	Arg	Phe	Cys	Ile	Asp	Ser	Glu	Asn	Arg		
		355					360					365					
Ile	Gly	Asn	Ser	Gly	Val	Glu	Glu	Ile	Lys	Gly	His	Pro	Phe	Phe	Glu		
	370					375				380							
Gly	Val	Asp	Trp	Glu	His	Ile	Arg	Glu	Arg	Pro	Ala	Ala	Ile	Pro	Ile		
385					390					395					400		
Glu	Ile	Lys	Ser	Ile	Asp	Asp	Thr	Ser	Asn	Phe	Asp	Asp	Phe	Pro	Glu		
			405					410						415			
Ser	Asp	Ile	Leu	Gln	Pro	Val	Pro	Asn	Thr	Thr	Glu	Pro	Asp	Tyr	Lys		
		420						425					430				
Ser	Lys	Asp	Trp	Val	Phe	Leu	Asn	Tyr	Thr	Tyr	Lys	Arg	Phe	Glu	Gly		
	435					440						445					
Leu	Thr	Gln	Arg	Gly	Ser	Ile	Pro	Thr	Tyr	Met	Lys	Ala	Gly	Lys	Leu		
	450					455					460						

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT06
- (B) CLONE: 827431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Leu	Leu	Leu	Lys	Lys	His	Thr	Glu	Asp	Ile	Ser	Ser	Val	Tyr	Glu		
1				5				10					15				
Ile	Arg	Glu	Arg	Leu	Gly	Ser	Gly	Ala	Phe	Ser	Glu	Val	Val	Leu	Ala		
		20						25				30					
Gln	Glu	Arg	Gly	Ser	Ala	His	Leu	Val	Ala	Leu	Lys	Cys	Ile	Pro	Lys		
	35						40					45					

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Lys Ala Leu Arg Gly Lys Glu Ala Leu Val Glu Asn Glu Ile Ala Val
 50          55          60
Leu Arg Arg Ile Ser His Pro Asn Ile Val Ala Leu Glu Asp Val His
65          70          75          80
Glu Ser Pro Ser His Leu Tyr Leu Ala Met Glu Leu Val Thr Gly Gly
      85          90          95
Glu Leu Phe Asp Arg Ile Met Glu Arg Gly Ser Tyr Thr Glu Lys Asp
      100          105          110
Ala Ser His Leu Val Gly Gln Val Leu Gly Ala Val Ser Tyr Leu His
      115          120          125
Ser Leu Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Tyr
      130          135          140
Ala Thr Pro Phe Glu Asp Ser Lys Ile Met Val Ser Asp Phe Gly Leu
      145          150          155          160
Ser Lys Ile Gln Ala Gly Asn Met Leu Gly Thr Ala Cys Gly Thr Pro
      165          170          175
Gly Tyr Val Ala Pro Glu Leu Leu Glu Gln Lys Pro Tyr Gly Lys Ala
      180          185          190
Val Asp Val Trp Ala Leu Gly Val Ile Ser Tyr Ile Leu Leu Cys Gly
      195          200          205
Tyr Pro Pro Phe Tyr Asp Glu Ser Asp Pro Glu Leu Phe Ser Gln Ile
      210          215          220
Leu Arg Ala Ser Tyr Glu Phe Asp Xaa Pro Phe Trp Asp Asp Ile Ser
      225          230          235          240
Glu Ser Gly Lys Asp Phe Ile Arg His Leu Leu Glu Arg Asp Leu Gln
      245          250          255
Lys Arg Phe Thr Cys Gln Gln Ala Leu Arg Asp Leu Trp Ile Phe Trp
      260          265          270
Asp Thr Gly Phe Gly Arg Asp Ile Leu Gly Phe Val Ser Glu Gln Ile
      275          280          285
Arg Lys Asn Phe Ala Trp Thr His Trp Lys Arg Ala Phe Asn Ala Thr
      290          295          300
Leu Phe Leu Arg His Ile Arg Lys Leu Gly Gln Ile Pro Glu Gly Glu
      305          310          315          320
Gly Ala Ser Glu Gln Gly Met Xaa Arg His Ser His Xaa Gly Leu Arg
      325          330          335
Ala Gly Gln Pro Pro Lys Trp
      340

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNTUT03
- (B) CLONE: 1340712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Ile Leu Ala Ser Val Leu Arg Ser Gly Pro Gly Gly Gly Leu Pro
 1          5          10          15
Leu Arg Pro Leu Leu Gly Pro Ala Leu Ala Leu Arg Ala Arg Ser Thr
      20          25          30
Ser Ala Thr Asp Thr His His Val Glu Met Ala Arg Glu Arg Ser Lys
      35          40          45
Thr Val Thr Ser Phe Tyr Asn Gln Ser Ala Ile Asp Ala Ala Ala Glu
      50          55          60
Lys Pro Ser Val Arg Leu Thr Pro Thr Met Met Leu Tyr Ala Gly Arg
      65          70          75          80
Ser Gln Asp Gly Ser His Leu Leu Lys Ser Ala Arg Tyr Leu Gln Gln
      85          90          95

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Glu Leu Pro Val Arg Ile Ala His Arg Ile Lys Gly Phe Arg Cys Leu
 100 105 110
 Pro Phe Ile Ile Gly Cys Asn Pro Thr Ile Leu His Val His Glu Leu
 115 120 125
 Tyr Ile Arg Ala Phe Gln Lys Leu Thr Asp Phe Pro Pro Ile Lys Asp
 130 135 140
 Gln Ala Asp Glu Ala Gln Tyr Cys Gln Leu Val Arg Gln Leu Leu Asp
 145 150 155 160
 Asp His Lys Asp Val Val Thr Leu Leu Ala Glu Gly Leu Arg Glu Ser
 165 170 175
 Arg Lys His Ile Glu Asp Glu Lys Leu Val Arg Tyr Phe Leu Asp Lys
 180 185 190
 Thr Leu Thr Ser Arg Leu Gly Ile Arg Met Leu Ala Thr His His Leu
 195 200 205
 Ala Leu His Glu Asp Lys Pro Asp Phe Val Gly Ile Ile Cys Thr Arg
 210 215 220
 Leu Ser Pro Lys Lys Ile Glu Lys Trp Val Asp Phe Ala Arg Arg
 225 230 235 240
 Leu Cys Glu His Lys Tyr Gly Asn Ala Pro Arg Val Arg Ile Asn Gly
 245 250 255
 His Val Ala Ala Arg Phe Pro Phe Ile Pro Met Pro Leu Asp Tyr Ile
 260 265 270
 Leu Pro Glu Leu Leu Lys Asn Ala Met Arg Ala Thr Met Glu Ser His
 275 280 285
 Leu Asp Thr Pro Tyr Asn Val Pro Asp Val Val Ile Thr Ile Ala Asn
 290 295 300
 Asn Asp Val Asp Leu Ile Ile Arg Ile Ser Asp Arg Gly Gly Gly Ile
 305 310 315 320
 Ala His Lys Asp Leu Asp Arg Val Met Asp Tyr His Phe Thr Thr Ala
 325 330 335
 Glu Ala Ser Thr Gln Asp Pro Arg Ile Ser Pro Leu Phe Gly His Leu
 340 345 350
 Asp Met His Ser Gly Ala Gln Ser Gly Pro Met His Gly Phe Gly Phe
 355 360 365
 Gly Leu Pro Thr Ser Arg Ala Tyr Ala Glu Tyr Leu Gly Gly Ser Leu
 370 375 380
 Gln Leu Gln Ser Leu Gln Gly Ile Gly Thr Asp Val Tyr Leu Arg Leu
 385 390 395 400
 Arg His Ile Asp Gly Arg Glu Glu Ser Phe Arg Ile
 405 410

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PENITUT01
- (B) CLONE: 1452972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Leu Glu Lys Leu Glu Phe Glu Asp Glu Ala Val Glu Asp Ser Glu
 1 5 10 15
 Ser Gly Val Tyr Met Arg Phe Met Arg Ser His Lys Cys Tyr Asp Ile
 20 25 30
 Val Pro Thr Ser Ser Lys Leu Val Val Phe Asp Thr Thr Leu Gln Val
 35 40 45
 Lys Lys Ala Phe Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro
 50 55 60

Leu	Trp	Glu	Ser	Lys	Lys	Gln	Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr		
65					70					75				80			
Asp	Phe	Ile	Asn	Ile	Leu	His	Arg	Tyr	Tyr	Lys	Ser	Pro	Met	Val	Gln		
			85					90						95			
Ile	Tyr	Glu	Leu	Glu	Glu	His	Lys	Ile	Glu	Thr	Trp	Arg	Glu	Leu	Tyr		
			100					105					110				
Leu	Gln	Glu	Thr	Phe	Lys	Pro	Leu	Val	Asn	Ile	Ser	Pro	Asp	Ala	Ser		
		115					120					125					
Leu	Phe	Asp	Ala	Val	Tyr	Ser	Leu	Ile	Lys	Asn	Lys	Ile	His	Arg	Leu		
	130					135					140						
Pro	Val	Ile	Asp	Pro	Ile	Ser	Gly	Asn	Ala	Leu	Tyr	Ile	Leu	Thr	His		
145					150					155					160		
Lys	Arg	Ile	Leu	Lys	Phe	Leu	Gln	Leu	Phe	Met	Ser	Asp	Met	Pro	Lys		
			165					170						175			
Pro	Ala	Phe	Met	Lys	Gln	Asn	Leu	Asp	Glu	Leu	Gly	Ile	Gly	Thr	Tyr		
		180					185					190					
His	Asn	Ile	Ala	Phe	Ile	His	Pro	Asp	Thr	Pro	Ile	Ile	Lys	Ala	Leu		
	195						200					205					
Asn	Ile	Phe	Val	Glu	Arg	Arg	Ile	Ser	Ala	Leu	Pro	Val	Val	Asp	Glu		
210					215						220						
Ser	Gly	Lys	Val	Val	Asp	Ile	Tyr	Ser	Lys	Phe	Asp	Val	Ile	Asn	Leu		
225					230					235				240			
Ala	Ala	Glu	Lys	Thr	Tyr	Asn	Asn	Leu	Asp	Ile	Thr	Val	Thr	Gln	Ala		
			245						250					255			
Leu	Gln	His	Arg	Ser	Gln	Tyr	Phe	Glu	Gly	Val	Val	Lys	Cys	Asn	Lys		
		260						265					270				
Leu	Glu	Ile	Leu	Glu	Thr	Ile	Val	Asp	Arg	Ile	Val	Arg	Ala	Glu	Val		
	275					280					285						
His	Arg	Leu	Val	Val	Val	Asn	Glu	Ala	Asp	Ser	Ile	Val	Gly	Ile	Ile		
290					295						300						
Ser	Leu	Ser	Asp	Ile	Leu	Gln	Ala	Leu	Ile	Leu	Thr	Pro	Ala	Gly	Ala		
305				310					315					320			
Lys	Gln	Lys	Glu	Thr	Glu	Thr	Glu										
			325														

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2770 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUVENOB01
 (B) CLONE: 39043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAGTCGGCAC	CAGAGGCAAG	GGTGCGAGGA	CCACGGCCGG	CTCGGACGTG	TGACCGCGCC	60
TAGGGGGTGG	CAGCGGGCAG	TGCGGGGCGG	CAAGGCGACC	ATGGAGCTTT	TGCGGACTAT	120
CACCTACCAG	CCAGCCGCCA	GCACCAAAAT	GTGCGAGCAG	GCGCTGGGCA	AGGGTTGCGG	180
AGCGGACTCG	AAGAAGAAGC	GGCCGCCGCA	GCCCCCGAG	GAATCGCAGC	CACCTCAGTC	240
CCAGGCGCAA	GTGCCCCCGG	CGGCCCCCTCA	CCACCATCAC	CACCATTCGC	ACTCGGGGCC	300
GGAGATCTCG	CGGATTATCG	TCGACCCAC	GACTGGGAAG	CGCTACTGCC	GGGGCAAAGT	360
GCTGGGAAAG	GGTGGCTTTG	CAAAATGTTA	CGAGATGACA	GATTTGACAA	ATAACAAAGT	420
CTACGCCGCA	AAAATTATTC	CTCACAGCAG	AGTAGCTAAA	CCTCATCAAA	GGGAAAAGAT	480
TGACAAAGAA	ATAGAGCTTC	ACAGAATTCT	TCATCATAAG	CATGTAGTGC	AGTTTTACCA	540
CTACTTCGAG	GACAAAGAAA	ACATTTACAT	TCTCTTGGAA	TACTGCAGTA	GAAGGTCAAT	600
GGCTCATATT	TTGAAAGCAA	GAAAGGTGTT	GACAGAGCCA	GAAGTTCGAT	ACTACCTCAG	660
GCAGATTGTG	TCTGGACTGA	AATACCTTCA	TGAACAAGAA	ATCTTGCACA	GAGATCTCAA	720
ACTAGGGAAC	TTTTTTTATTA	ATGAAGCCAT	GGAACTAAAA	GTTGGGGACT	TCGGTCTGGC	780
AGCCAGGCTA	GAACCCTTGG	AACACAGAAG	GAGAACGATA	TGTGGTACCC	CAAATTATCT	840
CTCTCCTGAA	GTCCTCAACA	AACAAGGACA	TGGCTGTGAA	TCAGACATTT	GGGCCCTGGG	900
CTGTGTAATG	TATACAATGT	TACTAGGGAG	GCCCCCATTT	GAAACTACAA	ATCTCAAAGA	960

AACTTATAGG	TGCATAAGGG	AAGCAAGGTA	TACAATGCCG	TCCTCATTGC	TGGCTCCTGC	1020
CAAGCACTTA	ATTGCTAGTA	TGTTGTCCAA	AAACCCAGAG	GATCGTCCCA	GTTTGGATGA	1080
CATCATTCGA	CATGACTTTT	TTTTGCAGGG	CTTCACTCCG	GACAGACTGT	CTTCTAGCTG	1140
TTGTCATACA	GTTCCAGATT	TCCACTTATC	AAGCCCAGCT	AAGAATTTCT	TTAAGAAAGC	1200
AGCTGCTGCT	CTTTTTGGTG	GCAAAAAAGA	CAAAGCAAGA	TATATTGACA	CACATAATAG	1260
AGTGTCTAAA	GAAGATGAAG	ACATCTACAA	GCTTAGGCAT	GATTTGAAAA	AGACTTCAAT	1320
AACTCAGCAA	CCCAGCAAAC	ACAGGACAGA	TGAGGAGCTC	CAGCCACCTA	CCACCACAGT	1380
TGCCAGGTCT	GGAACACCCG	CAGTAGAAAA	CAAGCAGCAG	ATTGGGGATG	CTATTGCGAT	1440
GATAGTCAGA	GGGACTCTTG	GCAGCTGTAG	CAGCAGCAGT	GAATGCCTTG	AAGACAGTAC	1500
CATGGGAAGT	GTTGCAGACA	CAGTGGCAAG	GGTTCCTCGG	GGATGTCTGG	AAAACATGCC	1560
GGAAGCTGAT	TGCATTCCCA	AAGAGCAGCT	GAGCACATCA	TTTCAGTGGG	TCACCAAATG	1620
GGTTGATTAC	TCTAACAAAT	ATGGCTTTGG	GTACCAGCTC	TCAGACCACA	CCGTCGGTGT	1680
CCTTTTCAAC	AATGGTGCTC	ACATGAGCCT	CCTTCCAGAC	AAAAAAACAG	CTCACTATTA	1740
CGCAGAGCTT	GGCCAATGCT	CAGTTTTCCT	AGCAACAGAT	GCTCCTGAGC	AATTTATTAG	1800
TCAAGTGACG	GTGCTGAAAT	ACTTTTCTCA	TTACATGGAG	GAGAACCTCA	TGGATGGTGG	1860
AGATCTGCCT	AGTGTACTG	ATATTCGAAG	ACCTCGGCTC	TACCTCCTTC	AGTGGCTAAA	1920
ATCTGATAAG	GCCCTAATGA	TGCTCTTTAA	TGATGGCACC	TTTCAGGTGA	ATTTCTACCA	1980
TGATCATACA	AAAATCATCA	TCTGTAGCCA	AAATGAAGAA	TACCTTCTCA	CCTACATCAA	2040
TGAGGATAGG	ATATCTACAA	CTTTCAGGCT	GACAACTCTG	CTGATGTCTG	GCTGTTTCATC	2100
AGAATTAAAA	AATCGAATGG	AATATGCCCT	GAACATGCTC	TTACAAAAGAT	GTAACGTAAA	2160
GACTTTTCGA	ATGGACCCTA	TGGGACTCCT	CTTTTCCACT	GTGAGATCTA	CAGGGAAGCC	2220
AAAAGAATGA	TCTAGAGTAT	GTTGAAGAAG	ATGGACATGT	GGTGGTACGA	AAACAATTCC	2280
CCTGTGGCCT	GCTGGACTGG	GTGGAACCAG	AACAGGCTAA	GGCATACAGT	TCTTGACTTT	2340
GGACAATCCA	AGAGTGAACC	AGAATGCAGT	TTTCCTTGAG	ATACCTGTTT	TAAAAGGTTT	2400
TTCAGACAAT	TTTGCAGAAA	GGTGCATTGA	TTCTTAAATT	CTCTCTGTTG	AGAGCATTTT	2460
AGCCAGAGGA	CTTTGGAACT	GTGAATATAC	TTCTTGAAGG	GGAGGGAGAA	GGGAGGAAGC	2520
TCCCATGTTG	TTTAAAGGCT	GTAATTGGAG	CAGCTTTTGG	CTGCGTAACT	GTGAACTATG	2580
GCCATATATA	ATTTTTTTTC	ATTAATTTTT	GAAGATACTT	GTGGCTGGAA	AAGTGCATTC	2640
CTTGTTAATA	AACTTTTTTAT	TTATTACAGC	CCAAAGAGCA	GTATTTATTA	TCAAAATGTC	2700
TTTTTTTTTTA	TGTTGACCAT	TTTAAACCGT	TGGCAATAAA	GAGTATGAAA	ACGCAGAAAA	2760
AAAAAAAAA						2770

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TBLYN01
- (B) CLONE: 40194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAGGCGTCC	CCTTCTACTC	ACGTTTGCCA	AAAGCGGGTC	CGACGTGTTA	GCGGAAAAAA	60
GTGATGCCAC	CAAAAAGAAA	TGAAAAATAC	AAACTTCCTA	TTCCATTTC	AGAAGGCAAG	120
GTTCTGGATG	ATATGGAAGG	CAATCAGTGG	GTACTGGGCA	AGAAGATTGG	CTCTGGAGGA	180
TTTGGATTGA	TATATTTAGC	TTTCCCACA	AATAAACCCAG	AGAAAGATGC	AAGACATGTA	240
GTAAGAGTGG	AATATCAAGA	AAATGGCCCG	TTATTTTCAG	AACTTAAATT	TTATCAGAGA	300
GTTGCAAAAA	AAGACTGTAT	CAAAAAGTGG	ATAGAACGCA	AACAACCTGA	TTATTTAGGA	360
ATTCTCTGT	TTTATGGATC	TGGTCTGACT	GAATTCAAGG	GAAGAAAGTTA	CAGATTTATG	420
GTAATGGAAA	GACTAGGAAT	AGATTTACAG	AAGATCTCAG	GCCAGAATGG	TACCTTTAAA	480
AAGTCAACTG	TCCTGCAATT	AGGTATCCGA	ATGTTGGATG	TACTGGAATA	TATACATGAA	540
AATGAATATG	TTTATGGTGA	TGTAAAAGCA	GCAATCTAC	TTTTGGGTTA	CAAAAATCCA	600
GACCAAGTTT	ATCTTGACAG	TTATGGACTT	TCCTACAGAT	ATTGTCCCAA	TGGGAACCAC	660
AAACAGTATC	AGGAAAATCC	TAGAAAAGGC	CATAATGGGA	CAATAGAGTT	TACCAGCTTG	720
GATGCCACAC	AGGGAGTAGG	TGAAATAGCC	CAATTTTGG	TATGTGCTCA	TAGTTTAGCA	780
TATGATGAAA	AGCCAACTA	TCAAGCCCTC	AAGAAAATTT	TGAACCTCA	TGGAATACCT	840
TTAGGACCAC	TGGACTTTTC	CACAAAAGGA	CAGAGTATAA	ATGTCCATAC	TCCAAACAGT	900
CAAAAAGTTG	ATTCACAAA	GGCTGCAACA	AAGCAAGTCA	ACAAGGCACA	CAATAGGTTA	960
ATCGAAAAAA	AAGTCCACAG	TGAGAGAAGC	GCTGAGTCCT	GTGCAACATG	GAAAGTGCAG	1020
AAAGAGGAGA	AACTGATTGG	ATTGATGAAC	AATGAAGCAG	CTCAGGAAAG	CACAAGGAGA	1080
AGACAGAAAT	ATCAAGAGTC	TCAAGAACCT	TTGAATGAAG	TAAACAGTTT	CCCACAAAAA	1140
ATCAGCTATA	CACAATTCCC	AAACTCATTT	TATGAGCCTC	ATCAAGATTT	TACCAGTCCA	1200

GATATATTCA	AGAAGTCAAG	ATCTCCATCT	TGGTATAAAT	ACACTTCCAC	AGTCAGCACG	1260
GGGATCACAG	ACTTAGAAAG	TTCAACTGGA	CTTTGGCCTA	CAATTTCCCA	GTTTACTCTT	1320
AGTGAAGAGA	CAAACGCAGA	TGTTTATTAT	TATCGCATCA	TCATACCTGT	CCTTTTGATG	1380
TTAGTATTTT	TTGCTTTATT	TTTTTCTCTGA	AGATGATACC	AAAATTCCCT	TTGATAATTT	1440
TTTAAGTTTC	CAGCTCTTCA	CCGAAATGTT	GTATTCTTAT	TTCAAGTGGT	CCTTCCAGAC	1500
ATTTTAAAG	TAATTGGCTT	TAAAAAGAGA	ACATATTTTA	ACAAAGTTTG	TGGACACTCT	1560
AAAAAATAAA	ATTGCTTTGT	ACTAGAAAAA	AAA			1593

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TMLR3DT01
- (B) CLONE: 402339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGCCCCGG	GAGCCCCGAT	GCTGGCCCCG	AGGAAGCCGG	TGCTGCCGGC	GCTCACCATC	60
AACCCTACCA	TCGCCGAGGG	CCCATCCCCCT	ACCAGCGAGG	GCGCCTCCGA	GGCAAACCTG	120
GTGGACCTGC	AGAAGAAGCT	GGAGGAGCTG	GAACCTTGACG	AGCAGCAGAA	GAAGCGGCTG	180
GAAGCCTTTT	TCACCCAGAA	AGCCAAGGTC	GGCGAACTCA	AAGACGATGA	CTTCGAAAGG	240
ATCTCAGAGC	TGGGCGCGGG	CAACGGCGGG	GTGGTCACCA	AAGTCCAGCA	CAGACCCTCG	300
GGCCTCATCA	TGGCCAGGAA	GCTGATCCAC	CTTGAGATCA	AGCCGGCCAT	CCGGAACCAG	360
ATCATCCGCG	AGCTGCAGGT	CCTGCACGAA	TGCAACTCGC	CGTACATCGT	GGGCTTCTAC	420
GGGGCCTTCT	ACAGTGACGG	GGAGATCAGC	ATTTGCATGG	AACACATGGA	CGGCGGCTCC	480
CTGGACCATC	TGCTGAAAGA	GGCCAAGAGG	ATTCCCGAGG	AGATCCTGGG	GAAAGTCAGC	540
ATCGCGGTTT	TCCGGGGCTT	GGCGTACCTC	CGAGAGAAAG	ACCAGATCAT	GCACCGAGAT	600
GTGAAGCCCT	CCAACATCCT	CGTGAACCTC	AGAGGGGAGA	TCAAGCTGTG	TGACTTCGGG	660
GTGAGCGGCC	AGCTCATCGA	CTCCATGGCC	AACTCCTTCG	TGGGCACGCG	CTCCTACATG	720
GCTCCGGAGC	GGTTGCAGGG	CACACATTAC	TCGGTGCAGT	CGGACATCTG	GAGCATGGGC	780
CTGTCCCTGG	TGGAGCTGGC	CGTCGGAAGG	TACCCCATCC	CCCCGCCCGA	CGCCAAAGAG	840
CTGGAGGCCA	TCTTTGGCCC	GCCCGTGGTC	GACGGGGAAG	AAGGAGAGCC	TCACAGCATC	900
TGCCTCGGC	CGAGGCCCCC	CGGGCGCCCC	GTGAGCGGTC	ACGGGATGGA	TAGCCGGCCT	960
GCCATGGCCA	TCTTTGAACT	CCTGGACTAT	ATTGTGAACG	AGCCACCTCC	TAAGCTGCCC	1020
AACGGTGTGT	TCACCCCCGA	CTTCCAGGAG	TTTGTCAATA	AATGCCTCAT	CAAGAACCCA	1080
GCGGAGCGGG	CGGACCTGAA	GATGCTCACA	AACCACACCT	TCATCAAGCG	GTCCGAGGTG	1140
GAAGAAGTGG	ATTTTGCCGG	CTGGTTGTGT	AAAACCCCTG	GGCTGAACCA	GCCCGGCACA	1200
CCCACGCGCA	CCGCCGTGTG	ACAGTGGCCC	GGCTCCCTGC	GTCCCGCTGG	TGACCTGCCC	1260
ACCGTCCCTG	TCCATGCCCC	GCCCTTCCAG	CTGAGGACAG	GCTGGCGCCT	CCACCCACCC	1320
TCCTGCCTCA	CCCCTGCGGA	GAGCACCGTG	GCGGGGCGAC	AGCGCATGCA	GGAACGGGGG	1380
TCTCCTCTCC	TGCCCCGTCCT	GGCCGGGGTG	CCTCTGGGGA	CGGGCGACGC	TGCTGTGTGT	1440
GGTCTCAGAG	GCTCTGCTTC	CTTAGGTTAC	AAAACAAAAC	AGGGAGAGAA	AAAGCAAAAA	1500
AAAA						1504

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1935 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT04
- (B) CLONE: 705365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGGAGGCTG	AGCCGGCCGC	GGGCGCGACC	GGAGGCAGTT	TCCGTTACTA	TGGCAATGAC	60
GGCAGGGACT	ACAACAACCT	TTCTATGAG	CAACCATACC	CGGGAAAGAG	TGACTGTAGC	120
CAAGCTCACA	TTGGAGAATT	TTTATAGCAA	CCTAATTTTA	CAGCATGAAG	AGAGAGAAAC	180

CAGGCAGAAG	AAATTAGAAG	TGGCCATGGA	AGAAGAAGGA	TTAGCAGATG	AAGAGAAAAA	240
GTTACGTCGA	TCACAACACG	CTCGCAAAGA	AACAGAGTTC	TTACGGCTCA	AAAGGACCAG	300
ACTTGGCTTG	GATGACTTTG	AGTCTCTGAA	AGTTATAGGA	AGAGGAGCTT	TTGGAGAGGT	360
GCGGTTGGTC	CACAAAAAAG	ATACAGGCCA	TATCTATGCA	ATGAAGATAT	TGAGAAAGTC	420
TGATATGCTT	GA AAAAGAGC	AGGTGGCCCA	TATCCGAGCA	GAAAGAGATA	TTTTGGTAGA	480
AGCAGATGGT	GCCTGGGTGG	TGAAGATGTT	TTACAGTTTT	CAGGATAAGA	GGAATCTTTA	540
TCTAATCATG	GAATTTCTCC	CTGGAGGTGA	CATGATGACA	TTGCTAATGA	AGAAAGACAC	600
CTTGACAGAA	GAGGAAACAC	AGTTCTACAT	TTCAGAGACT	GTTCTGGCAA	TAGATGCGAT	660
CCACCAGTTG	GGTTTCATCC	ATCGGGATAT	TAAGCCAGAC	AACCTTTTAT	TGGATGCCAA	720
GGGTCAATGA	AAATTATCTG	ATTTTGGTTC	ATGTACGGGA	TTAAAGAAAG	CTCACAGGAC	780
TGAATTTTAT	AGAAATCTCA	CACACAACCC	ACCAAGTGAC	TTCTCATTTT	AGAACATGAA	840
CTCAAAGAGG	AAAGCAGAAA	CTTGAAGAA	GAACAGGAGA	CAACTGGCAT	ATTCCACAGT	900
TGGGACACCA	GATTACATTG	CTCCAGAAGT	ATTCATGCAG	ACTGGTTACA	ACAAATTGTG	960
TGACTGGTGG	TCTTTGGGAG	TGATTATGTA	TGAAATGCTA	ATAGGATATC	CACCTTTCTG	1020
CTCTGAAACA	CCTCAAGAAA	CATACAGAAA	AGTGATGAAC	TGGAAAGAAA	CTCTGGTATT	1080
TCCTCCAGAG	GTACCTATAT	CTGAGAAAGC	CAAGGACTTA	ATTCTCAGAT	TTTGTATTGA	1140
TTCTGAAAAC	AGAATTGGAA	ATAGTGGAGT	AGAAGAAATA	AAAGGTCATC	CCTTTTTTGA	1200
AGGTGTCGAC	TGGGAGCACA	TAAGGGAAAG	GCCAGCAGCA	ATCCCTATAG	AAATCAAAAG	1260
CATTGATGAT	ACTTCAAATT	TTGATGACTT	CCCTGAATCT	GATATTTTAC	AACCAGTGCC	1320
AAATACCACA	GAACCGGACT	ACAAATCCAA	AGACTGGGTT	TTTCTCAATT	ATACCTATAA	1380
AAGGTTTGAA	GGGTTGACTC	AACGTGGCTC	TATCCCCACC	TACATGAAAG	CTGGGAAGTT	1440
ATGAATGAAG	ATAACATTCA	CCCATAACCA	AGAGAAGTCA	GGTAGCTGCA	TCACCAGGCT	1500
TGCTTGGCGT	AGATAACAAT	ACACTGAAAT	ACTCCTGAAG	ATGGTGGTGC	TTATTGACTA	1560
CAAGAGGAAA	TTCTACAGGA	TTAGGATTTT	TAAGACTACT	ATAGGAATTG	GTTGGCAGTG	1620
CCAGCTGGCT	CTTTTTTTTA	ATATTTTATT	ATTTTGTGTA	ACTTTATTAT	ATGAAGGTAC	1680
TGGAATAAAA	GGAACAGACA	TCCCTTTCTA	ACTGCACTGC	CTACATGCGT	ATTAAGGTCC	1740
ATTCTGCCTG	TGTGTGCTGT	GGCTTTGAAC	TGTAACACCT	CTAATCAATT	CAGGAGAAAC	1800
ACATATCATT	TAAAGCAACA	TAGGCTAACC	TGTANGTAAC	ACTGCAGTAT	TGATGTTTTA	1860
CTGCAAATCT	TATGGGTCTA	GATAATCAGT	AAAAGCCATC	TTCCATAGTT	GGTGTTAGAA	1920
CATTGCCCTA	TTGGT					1935

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT06
- (B) CLONE: 827431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAAGTTTCTC	ACTAGGGTCT	TCTCTGGCCC	AGCCTTTGAC	TGAAGCTGGT	CTGGAGACAG	60
GGGCATTAGA	GAAGTGACTC	ATAGATGGCC	TAAAGAAGCG	GGGCCACTCA	AGGACCCAGG	120
ACAGAGGGAA	GAGGGCCAAC	CCAGCTGGAC	CACAGGCAAA	CCCCATTGCC	TTTGAGAGAA	180
AGAAGAGGAC	CCGGTGAAAC	ATGCTGCTGC	TGAAGAAACA	CACGGAGGAC	ATCAGCAGCG	240
TCTACGAGAT	CCGCGAGAGG	CTCGGCTCGG	GTGCCTTCTC	CGAGGTGGTG	CTGGCCCAGG	300
AGCGGGGCTC	CGCACACCTC	GTGGCCCTCA	AGTGCATCCC	CAAGAAGGCC	CTCCGGGGCA	360
AGGAGGCCCT	GGTGGAGAAC	GAGATCGCAG	TGCTCCGTAG	GATCAGTCAC	CCCAACATCG	420
TCGCTCTGGA	GGATGTCCAC	GAGAGCCCTT	CCCACCTCTA	CCTGGCCATG	GAAGTGGTGA	480
CGGGTGGCGA	GCTGTTTGAC	CGCATCATGG	AGCGCGGCTC	CTACACAGAG	AAGGATGCCA	540
GCCATCTGGT	GGGTCAGGTC	CTTGGCGCCG	TCTCCTACCT	GCACAGCCTG	GGGATCGTGC	600
ACCGGGACCT	CAAGCCCGAA	AACCTCCTGT	ATGCCACGCC	CTTTGAGGAC	TCGAAGATCA	660
TGGTCTCTGA	CTTTGGACTC	TCCAAAATCC	AGGCTGGGAA	CATGCTAGGC	ACCGCCTGTG	720
GGACCCCTGG	ATATGTGGCC	CCAGAGCTCT	TGGAGCAGAA	ACCCTACGGG	AAGGCCGTAG	780
ATGTGTGGGC	CCTGGGCGTC	ATCTCCTACA	TCCTGCTGTG	TGGGTACCCC	CCCTTCTACG	840
ACGAGAGCGA	CCCTGAGCTC	TTCAGCCAGA	TCCTGAGGGC	CAGCTATGAG	TTTGACTTNT	900
CTTTCTGGGA	TGACATCTCA	GAATCAGGCA	AAGACTTTAT	TCGGCACCTT	CTGGAGCGAG	960
ACCTTCAGAA	GAGGTTTACC	TGCCAACAGG	CCTTGCGGGA	CCTTTGGATC	TTTTGGGACA	1020
CAGGCTTTGG	CAGGGACATC	TTAGGGTTTG	TCAGTGAGCA	GATCCGGAAG	AACCTTGCTT	1080
GGACACACTG	GAAGCGAGCC	TTCAATGCCA	CCTTGTTTCT	GCGCCACATC	CGGAAGCTGG	1140
GGCAGATCCC	AGAGGGCGAG	GGGGCCTCTG	AGCAGGGCAT	GGSCCGNCAC	AGCCACTNAG	1200
GCCTTCGTGC	TGGCCAGCCC	CCCAAGTGGT	GATGCCCAGG	NAGATGCCGA	GGCCAAGTGG	1260

ANTGANCCCC AGATTNCTT NC

1282

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNTUT03
- (B) CLONE: 1340712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGCGGAGGG	CGCAGGCGGC	TGGGCGCCTG	GCGAGTGGAC	TGTTTCGAGCC	CTTCCGCTGG	60
GACCCGGGCC	CTGGCTCCGG	CCCCGCGATG	GGAGCTGCTC	TCCGCGGGCT	GAGCCTGTCA	120
GCATCCTCGA	CGCACCCTGG	TCCCTGAAGT	CGGAGAAGAG	CCCCTACCCA	CCCACACCCC	180
CTTGCCCCAT	TTTGGGTCGC	CTGGGTCCCT	AGTCCTAGCG	GATCCTCAGT	CCTAGCGGCC	240
ACCGGGTCTG	AAAGGAGCAA	GACGATGATC	CTGGCGTCGG	TGCTGAGGAG	CGGTCCCGGG	300
GGCGGGCTTC	CGTCCGGGCC	CCTCCTGGGA	CCCGCACTCG	CGCTCCGGGC	CCGCTCGACG	360
TCGGCCACCG	ACACACACCA	CGTGAGATG	GCTCGGGAGC	GCTCCAAGAC	CGTCACCTCC	420
TTTTACAACC	AGTCGGCCAT	CGACGCGGCA	GCGGAGAAGC	CCTCAGTCCG	CCTAACGCCC	480
ACCATGATGC	TCTACGCTGG	CCGCTCTCAG	GACGGCAGCC	ACCTTCTGAA	AAGTGCTCGG	540
TACCTGCAGC	AAGAACTTCC	AGTGAGGATT	GCTCACCGCA	TCAAGGGCTT	CCGCTGCCTT	600
CCTTTCATCA	TTGGCTGCAA	CCCCACCATA	CTGCACGTGC	ATGAGCTATA	TATCCGTGCC	660
TTCCAGAAGC	TGACAGACTT	CCCTCCGATC	AAGGACCAGG	CGGACGAGGC	CCAGTACTGC	720
CAGCTGGTGC	GACAGCTGCT	GGATGACCAC	AAGGATGTGG	TGACCCTCTT	GGCAGAGGGC	780
CTACGTGAGA	GCCGGAAGCA	CATAGAGGAT	GAAAAGCTCG	TCCGCTACTT	CTTGGACAAG	840
ACGCTGACTT	CGAGGCTTGG	AATCCGCATG	TTGGCCACGC	ATCACCTGGC	GCTGCATGAG	900
GACAAGCCTG	ACTTTGTCCG	CATCATCTGT	ACTCGTCTCT	CACCAAAGAA	GATTATTGAG	960
AAGTGGGTGG	ACTTTGCCAG	ACGCCGTGTG	GAGCACAAGT	ATGGCAATGC	GCCCCGTGTC	1020
CGCATCAATG	GCCATGTGGC	TGCCCGGTTC	CCCTTCATCC	CTATGCCACT	GGACTACATC	1080
CTGCCGGAGC	TGCTCAAGAA	TGCCATGAGA	GCCACAATGG	AGAGCCACCT	AGACACTCCC	1140
TACAATGTCC	CAGATGTGGT	CATCACCATC	GCCAACAATG	ATGTCGATCT	GATCATCAGG	1200
ATCTCAGACC	GTGGTGGAGG	AATCGCTCAC	AAAGATCTGG	ACCGGGTCAT	GGACTACCAC	1260
TTCATGATC	CTGAGGCCAG	CACACAGGAC	CCCCGGATCA	GCCCCCTCTT	TGGCCATCTG	1320
GACATGCATA	GTGGCGCCCA	GTCAGGACCC	ATGCACGGCT	TTGGCTTCGG	GTTGCCCACG	1380
TCACGGGCCCT	ACGCGGAGTA	CCTCGGTGGG	TCTCTGCAGC	TGCAGTCCCT	GCAGGGCATT	1440
GGCACGGAGC	TCTACCTGCG	GCTCCGCCAC	ATCGATGGCC	GGGAGGAAAG	CTTCCGGATC	1500
TGACCCACAC	GCCTTTGGCC	TGCTCACCCG	ACCAGCCTGG	GCCGCATTCC	CTGCAGGACC	1560
TCCCGGGTCA	GGCAGGGCGG	CCCCTGCTC	CACACACTGC	TGCATCTTGG	GTCTCAGGGA	1620
CCCAGACAGA	TGGACTTACA	TGGAGCTGGG	CACTGCCCCC	GCCTCAACAG	GGTCCATTGC	1680
TCTCTCGCCT	CAGAACTTGG	AGCAGGGAAG	TGGGCACCTG	AGGCCTCAGC	ACAGTGTCGT	1740
CATTCTCTTC	TGGGGGACCC	CACTCTGAGC	TGTTATTAAA	GTTACATTTT	TGGAATGGCC	1800
AGAAAAGAAG	GAAGGTGGAT	GGTGGTGAGG	AGGGGTGGGG	AGAGGTGAGG	TGGTTGTGGT	1860
TTGTGT						1866

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PENITUT01
- (B) CLONE: 1452972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCCCCAGCG	CTCGGCCGGC	CGCGAGCCCC	CCGGCCGGGG	ACGAGCGTCG	CAGCTCATGC	60
TGATCGCTGT	CCTCCTCCTC	CCCCTCAGGC	GGCGCTGGCG	GCGGCCCTGG	GACCCGCGGA	120
AGCCGGCATG	CTGGAGAAGC	TGGAGTTCGA	GGACGAAGCA	GTAAGAAGACT	CAGAAAGTGG	180

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TGTTTACATG CGATTTCATGA GGTACACACAA GTGTTATGAC ATCGTTCCAA CCAGTTCAAA 240
GCTTGTTGTC TTTGATACTA CATTACAAGT TAAAAAGGCC TTCTTTGCTT TGGTAGCCAA 300
CGGTGTCCGA GCAGCGCCAC TGTGGGAGAG TAAAAACAA AGTTTTGTAG GAATGCTAAC 360
AATTACAGAT TTCATAAATA TACTACATAG ATACTATAAA TCACCTATGG TACAGATTTA 420
TGAATTAGAG GAACATAAAA TTGAAACATG GAGGGAGCTT TATTTACAAG AAACATTTAA 480
GCCTTTAGTG AATATATCTC CAGATGCAAG CCTCTTCGAT GCTGTATACT CCTTGATCAA 540
AAATAAAATC CACAGATTGC CCGTTATTGA CCCTATCAGT GGAATGCAC TTTATATACT 600
TACCCACAAA AGAATCCTCA AGTTCCTCCA GCTTTTTATG TCTGATATGC CAAAGCCTGC 660
CTTCATGAAG CAGAACCTGG ATGAGCTTGG AATAGGAACG TACCACAACA TTGCCTTCAT 720
ACATCCAGAC ACTCCCATCA TCAAAGCCTT GAACATATTT GTGGAAAGAC GAATATCAGC 780
TCTGCCTGTT GTGGATGAGT CAGGAAAAGT TGATAGATATT TATTCCAAAT TTGATGTAAT 840
TAATCTTGCT GCTGAGAAAA CATACAATAA CCTAGATATC ACGGTGACCC AGGCCCTTCA 900
GCACCGTTCA CAGTATTTTG AAGGTGTTGT GAAGTGCAAT AAGCTGGAAA TACTGGAGAC 960
CATCGTGGAC AGAATAGTAA GAGCTGAGGT CCATCGGCTG GTGGTGGTAA ATGAAGCAGA 1020
TAGTATTGTG GGTATTATTT CCCTGTCGGA CATTCTGCAA GCCCTGATCC TCACACCAGC 1080
AGGTGCCAAA CAAAAGGAGA CAGAAACGGA GTGACCGCCG TGAATGTAGA CGCCCTAGGA 1140
GGAGAACTTG AACAAAGTCT CTGGGTCACG TTTTGCCTCA TGAACACTGG CTGCAAGTGG 1200
TTAAGAATGT ATATCAGGGT TTAACAATAG GTATTTCTTC CAGTGATGTT GAAATTAAGC 1260
TTAAAAAGA AAGATTTTAT TGCTTGAAG ATTCAGGCTT GCATTAAAAG ACTGTTTTCA 1320
GACCTTTGTC TGAAGGATTT TAAATGCTGT ATGTCATTAA AGTGCACGTG GTCCTGAAGT 1380
TTTCATTATT TTTCATTTC AAGAATTCAC TGGTATGGAA CAGGTGATGT GGCAT 1435

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1488263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Met Leu Ala Gly Leu Pro Thr Ser Asp Pro Gly Arg Leu Ile Thr Asp
 1          5          10          15
Pro Arg Ser Gly Arg Thr Tyr Leu Lys Gly Arg Leu Leu Gly Lys Gly
 20          25          30
Gly Phe Ala Arg Cys Tyr Glu Ala Thr Asp Thr Glu Thr Gly Ser Ala
 35          40          45
Tyr Ala Val Lys Val Ile Pro Gln Ser Arg Val Ala Lys Pro His Gln
 50          55          60
Arg Glu Lys Ile Leu Asn Glu Ile Glu Leu His Arg Asp Leu Gln His
 65          70          75          80
Arg His Ile Val Arg Phe Ser His His Phe Glu Asp Ala Asp Asn Ile
 85          90          95
Tyr Ile Phe Leu Glu Leu Cys Ser Arg Lys Ser Leu Ala His Ile Trp
100          105          110
Lys Ala Arg His Thr Leu Leu Glu Pro Glu Val Arg Tyr Tyr Leu Arg
115          120          125
Gln Ile Leu Ser Gly Leu Lys Tyr Leu His Gln Arg Gly Ile Leu His
130          135          140
Arg Asp Leu Lys Leu Gly Asn Phe Phe Ile Thr Glu Asn Met Glu Leu
145          150          155          160
Lys Val Gly Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Pro Glu Gln
165          170          175
Arg Lys Lys Thr Ile Cys Gly Thr Pro Asn Tyr Val Ala Pro Glu Val
180          185          190
Leu Leu Arg Gln Gly His Gly Pro Glu Ala Asp Val Trp Ser Leu Gly
195          200          205
Cys Val Met Tyr Thr Leu Leu Cys Gly Ser Pro Pro Phe Glu Thr Ala
210          215          220
Asp Leu Lys Glu Thr Tyr Arg Cys Ile Lys Gln Val His Tyr Thr Leu
225          230          235          240

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Pro Ala Ser Leu Ser Leu Pro Ala Arg Gln Leu Leu Ala Ala Ile Leu
      245      250      255
Arg Ala Ser Pro Arg Asp Arg Pro Ser Ile Asp Gln Ile Leu Arg His
      260      265      270
Asp Phe Phe Thr Lys Gly Tyr Thr Pro Asp Arg Leu Pro Ile Ser Ser
      275      280      285
Cys Val Thr Val Pro Asp Leu Thr Pro Pro Asn Pro Ala Arg Ser Leu
      290      295      300
Phe Ala Lys Val Thr Lys Ser Leu Phe Gly Arg Lys Lys Lys Ser Lys
      305      310      315      320
Asn His Ala Gln Glu Arg Asp Glu Val Ser Gly Leu Val Ser Gly Leu
      325      330      335
Met Arg Thr Ser Val Gly His Gln Asp Ala Arg Pro Glu Ala Pro Ala
      340      345      350
Ala Ser Gly Pro Ala Pro Val Ser Leu Val Glu Thr Ala Pro Glu Asp
      355      360      365
Ser Ser Pro Arg Gly Thr Leu Ala Ser Ser Gly Asp Gly Phe Glu Glu
      370      375      380
Gly Leu Thr Val Ala Thr Val Val Glu Ser Ala Leu Cys Ala Leu Arg
      385      390      395      400
Asn Cys Ile Ala Phe Met Pro Pro Ala Glu Gln Asn Pro Ala Pro Leu
      405      410      415
Ala Gln Pro Glu Pro Leu Val Trp Val Ser Lys Trp Val Asp Tyr Ser
      420      425      430
Asn Lys Phe Gly Phe Gly Tyr Gln Leu Ser Ser Arg Arg Val Ala Val
      435      440      445
Leu Phe Asn Asp Gly Thr His Met Ala Leu Ser Ala Asn Arg Lys Thr
      450      455      460
Val His Tyr Asn Pro Thr Ser Thr Lys His Phe Ser Phe Ser Val Gly
      465      470      475      480
Ala Val Pro Arg Ala Leu Gln Pro Gln Leu Gly Ile Leu Arg Tyr Phe
      485      490      495
Ala Ser Tyr Met Glu Gln His Leu Met Lys Gly Gly Asp Leu Pro Ser
      500      505      510
Val Glu Glu Val Glu Val Pro Ala Pro Pro Leu Leu Leu Gln Trp Val
      515      520      525

Lys Thr Asp Gln Ala Leu Leu Met Leu Phe Ser Asp Gly Thr Val Gln
      530      535      540
Val Asn Phe Tyr Gly Asp His Thr Lys Leu Ile Leu Ser Gly Trp Glu
      545      550      555      560
Pro Leu Leu Val Thr Phe Val Ala Arg Asn Arg Ser Ala Cys Thr Tyr
      565      570      575
Leu Ala Ser His Leu Arg Gln Leu Gly Cys Ser Pro Asp Leu Arg Gln
      580      585      590
Arg Leu Arg Tyr Ala Leu Arg Leu Leu Arg Asp Arg Ser Pro Ala
      595      600      605

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1827450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Pro Arg Val Lys Ala Ala Gln Ala Gly Arg Gln Ser Ser Ala Lys
  1      5      10      15
Arg His Leu Ala Glu Gln Phe Ala Val Gly Glu Ile Ile Thr Asp Met
      20      25      30

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Ala Lys Lys Glu Trp Lys Val Gly Leu Pro Ile Gly Gln Gly Gly Phe
      35              40              45
Gly Cys Ile Tyr Leu Ala Asp Met Asn Ser Ser Glu Ser Val Gly Ser
      50              55              60
Asp Ala Pro Cys Val Val Lys Val Glu Pro Ser Asp Asn Gly Pro Leu
65      70      75      80
Phe Thr Glu Leu Lys Phe Tyr Gln Arg Ala Ala Lys Pro Glu Gln Ile
      85              90              95
Gln Lys Trp Ile Arg Thr Arg Lys Leu Lys Tyr Leu Gly Val Pro Lys
      100      105      110

Tyr Trp Gly Ser Gly Leu His Asp Lys Asn Gly Lys Ser Tyr Arg Phe
      115      120      125
Met Ile Met Asp Arg Phe Gly Ser Asp Leu Gln Lys Ile Tyr Glu Ala
      130      135      140
Asn Ala Lys Arg Phe Ser Arg Lys Thr Val Leu Gln Leu Ser Leu Arg
145      150      155      160
Ile Leu Asp Ile Leu Glu Tyr Ile His Glu His Glu Tyr Val His Gly
      165      170      175
Asp Ile Lys Ala Ser Asn Leu Leu Leu Asn Tyr Lys Asn Pro Asp Gln
      180      185      190
Val Tyr Leu Val Asp Tyr Gly Leu Ala Tyr Arg Tyr Cys Pro Glu Gly
      195      200      205
Val His Lys Glu Tyr Lys Glu Asp Pro Lys Arg Cys His Asp Gly Thr
210      215      220
Ile Glu Phe Thr Ser Ile Asp Ala His Asn Gly Val Ala Pro Ser Arg
225      230      235      240
Arg Gly Asp Leu Glu Ile Leu Gly Tyr Cys Met Ile Gln Trp Leu Thr
      245      250      255
Gly His Leu Pro Trp Glu Asp Asn Leu Lys Asp Pro Lys Tyr Val Arg
      260      265      270
Asp Ser Lys Ile Arg Tyr Arg Glu Asn Ile Ala Ser Leu Met Asp Lys
      275      280      285
Cys Phe Pro Glu Lys Asn Lys Pro Gly Glu Ile Ala Lys Tyr Met Glu
290      295      300
Thr Val Lys Leu Leu Asp Tyr Thr Glu Lys Pro Leu Tyr Glu Asn Leu
305      310      315      320
Arg Asp Ile Leu Leu Gln Gly Leu Lys Ala Ile Gly Ser Lys Asp Asp
      325      330      335
Gly Lys Leu Asp Leu Ser Val Val Glu Asn Gly Gly Leu Lys Ala Lys
      340      345      350
Thr Ile Thr Lys Lys Arg Lys Lys Glu Ile Glu Glu Ser Lys Glu Pro
      355      360      365
Gly Val Glu Asp Thr Glu Trp Ser Asn Thr Gln Thr Glu Glu Ala Ile
370      375      380
Gln Thr Arg Ser Arg Thr Arg Lys Arg Val Gln Lys
385      390      395

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 303804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro
 1          5          10          15
Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala

```


[illegible]

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
(B) CLONE: 8541070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Met Thr Gly Ser Thr Pro Cys Ser Ser Met Ser Asn His Thr
1 5 10 15

Lys Glu Arg Val Thr Met Thr Lys Val Thr Leu Glu Asn Phe Tyr Ser
 20 25 30
 Asn Leu Ile Ala Gln His Glu Glu Arg Glu Met Arg Gln Lys Lys Leu
 35 40 45
 Glu Lys Val Met Glu Glu Glu Gly Leu Lys Asp Glu Glu Lys Arg Leu
 50 55 60
 Arg Arg Ser Ala His Ala Arg Lys Glu Thr Glu Phe Leu Arg Leu Lys
 65 70 75 80
 Arg Thr Arg Leu Gly Leu Glu Asp Phe Glu Ser Leu Lys Val Ile Gly
 85 90 95
 Arg Gly Ala Phe Gly Glu Val Arg Leu Val Gln Lys Lys Asp Thr Gly
 100 105 110

 His Val Tyr Ala Met Lys Ile Leu Arg Lys Ala Asp Met Leu Glu Lys
 115 120 125
 Glu Gln Val Gly His Ile Arg Ala Glu Arg Asp Ile Leu Val Glu Ala
 130 135 140
 Asp Ser Leu Trp Val Val Lys Met Phe Tyr Ser Phe Gln Asp Lys Leu
 145 150 155 160
 Asn Leu Tyr Leu Ile Met Glu Phe Leu Pro Gly Gly Asp Met Met Thr
 165 170 175
 Leu Leu Met Lys Lys Asp Thr Leu Thr Glu Glu Glu Thr Gln Phe Tyr
 180 185 190
 Ile Ala Glu Thr Val Leu Ala Ile Asp Ser Ile His Gln Leu Gly Phe
 195 200 205
 Ile His Arg Asp Ile Lys Pro Asp Asn Leu Leu Leu Asp Ser Lys Gly
 210 215 220
 His Val Lys Leu Ser Asp Phe Gly Leu Cys Thr Gly Leu Lys Lys Ala
 225 230 235 240
 His Arg Thr Glu Phe Tyr Arg Asn Leu Asn His Ser Leu Pro Ser Asp
 245 250 255
 Phe Thr Phe Gln Asn Met Asn Ser Lys Arg Lys Ala Glu Thr Trp Lys
 260 265 270
 Arg Asn Arg Arg Gln Leu Ala Phe Ser Thr Val Gly Thr Pro Asp Tyr
 275 280 285
 Ile Ala Pro Glu Val Phe Met Gln Thr Gly Tyr Asn Lys Leu Cys Asp
 290 295 300
 Trp Trp Ser Leu Gly Val Ile Met Tyr Glu Met Leu Ile Gly Tyr Pro
 305 310 315 320
 Pro Phe Cys Ser Glu Thr Pro Gln Glu Thr Tyr Lys Lys Val Met Asn
 325 330 335
 Trp Lys Glu Thr Leu Thr Phe Pro Pro Glu Val Pro Ile Ser Glu Lys
 340 345 350
 Ala Lys Asp Leu Ile Leu Arg Phe Cys Cys Glu Trp Glu His Arg Ile
 355 360 365
 Gly Ala Pro Gly Val Glu Glu Ile Lys Ser Asn Ser Phe Phe Glu Gly
 370 375 380
 Val Asp Trp Glu His Ile Arg Glu Arg Pro Ala Ala Ile Ser Ile Glu
 385 390 395 400
 Ile Lys Ser Ile Asp Asp Thr Ser Asn Phe Asp Glu Phe Pro Glu Ser
 405 410 415
 Asp Ile Leu Lys Pro Thr Val Ala Thr Ser Asn His Pro Glu Thr Asp
 420 425 430

 Tyr Lys Asn Lys Asp Trp Val Phe Ile Asn Tyr Thr Tyr Lys Arg Phe
 435 440 445
 Glu Gly Leu Thr Ala Arg Gly Ala Ile Pro Ser Tyr Met Lys Ala Ala
 450 455 460
 Lys
 465

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 790790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Leu Gly Ala Val Glu Gly Pro Arg Trp Lys Gln Ala Glu Asp Ile
 1          5          10          15
Arg Asp Ile Tyr Asp Phe Arg Asp Val Leu Gly Thr Gly Ala Phe Ser
 20          25          30

Glu Val Ile Leu Ala Glu Asp Lys Arg Thr Gln Lys Leu Val Ala Ile
 35          40          45
Lys Cys Ile Ala Lys Glu Ala Leu Glu Gly Lys Glu Gly Ser Met Glu
 50          55          60
Asn Glu Ile Ala Val Leu His Lys Ile Lys His Pro Asn Ile Val Ala
 65          70          75          80
Leu Asp Asp Ile Tyr Glu Ser Gly Gly His Leu Tyr Leu Ile Met Gln
 85          90          95
Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu Lys Gly Phe
100          105          110
Tyr Thr Glu Arg Asp Ala Ser Arg Leu Ile Phe Gln Val Leu Asp Ala
115          120          125
Val Lys Tyr Leu His Asp Leu Gly Ile Val His Arg Asp Leu Lys Pro
130          135          140
Glu Asn Leu Leu Tyr Tyr Ser Leu Asp Glu Asp Ser Lys Ile Met Ile
145          150          155          160
Ser Asp Phe Gly Leu Ser Lys Met Glu Asp Pro Gly Ser Val Leu Ser
165          170          175
Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala Gln
180          185          190
Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile Ala
195          200          205
Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu Asn Asp Ala
210          215          220
Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe Asp Ser Pro
225          230          235          240
Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile Arg His Leu
245          250          255
Met Glu Lys Asp Pro Glu Lys Arg Phe Thr Cys Glu Gln Ala Leu Gln
260          265          270
His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asp Lys Asn Ile His Gln
275          280          285
Ser Val Ser Glu Gln Ile Lys Lys Asn Phe Ala Lys Ser Lys Trp Lys
290          295          300
Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg Lys Leu Gln
305          310          315          320
Leu Gly Thr Ser Gln Glu Gly Gln Gly Gln Thr Ala Ser His Gly Glu
325          330          335

Leu Leu Thr Pro Val Ala Gly Gly Pro Ala Ala Gly Cys Cys Cys Arg
340          345          350
Asp Cys Cys Val Glu Pro Gly Thr Glu Leu Ser Pro Thr Leu Pro His
355          360          365
Gln Leu
370

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 924921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser	Thr	Ser	Ala	Thr	Asp	Thr	His	His	Val	Glu	Leu	Ala	Arg	Glu	Arg	1	5	10	15
Ser	Lys	Thr	Val	Thr	Ser	Phe	Tyr	Asn	Gln	Ser	Ala	Ile	Asp	Val	Val	20	25	30	
Ala	Glu	Lys	Pro	Ser	Val	Arg	Leu	Thr	Pro	Thr	Met	Met	Leu	Tyr	Ser	35	40	45	
Gly	Arg	Ser	Gln	Asp	Gly	Ser	His	Leu	Leu	Lys	Ser	Gly	Arg	Tyr	Leu	50	55	60	
Gln	Gln	Glu	Leu	Pro	Val	Arg	Ile	Ala	His	Arg	Ile	Lys	Gly	Phe	Arg	65	70	75	80
Ser	Leu	Pro	Phe	Ile	Gly	Cys	Asn	Pro	Thr	Ile	Leu	His	Val	His		85	90	95	
Glu	Leu	Tyr	Ile	Arg	Ala	Phe	Gln	Lys	Leu	Thr	Asp	Phe	Pro	Pro	Ile	100	105	110	
Lys	Asp	Gln	Ala	Asp	Glu	Ala	Gln	Tyr	Cys	Gln	Leu	Val	Arg	Gln	Leu	115	120	125	
Leu	Asp	Asp	His	Lys	Asp	Val	Thr	Leu	Leu	Ala	Glu	Gly	Leu	Arg		130	135	140	
Glu	Ser	Arg	Lys	His	Ile	Glu	Asp	Glu	Lys	Leu	Val	Arg	Tyr	Phe	Leu	145	150	155	160
Asp	Lys	Thr	Leu	Thr	Ser	Arg	Leu	Gly	Ile	Arg	Met	Leu	Ala	Thr	His	165	170	175	
His	Leu	Ala	Leu	His	Glu	Asp	Lys	Pro	Asp	Phe	Val	Gly	Ile	Ile	Cys	180	185	190	
Thr	Arg	Leu	Ser	Pro	Lys	Lys	Ile	Ile	Glu	Lys	Trp	Val	Asp	Phe	Ala	195	200	205	
Arg	Arg	Leu	Cys	Glu	His	Lys	Tyr	Gly	Asn	Ala	Pro	Arg	Val	Arg	Ile	210	215	220	
Asn	Gly	His	Val	Ala	Ala	Arg	Phe	Pro	Phe	Ile	Pro	Met	Pro	Leu	Asp	225	230	235	240
Tyr	Ile	Leu	Pro	Glu	Leu	Leu	Lys	Asn	Ala	Met	Arg	Ala	Thr	Met	Glu	245	250	255	
Ser	His	Leu	Asp	Thr	Pro	Tyr	Asn	Val	Pro	Asp	Val	Val	Ile	Thr	Ile	260	265	270	
Ala	Asn	Asn	Asp	Val	Asp	Leu	Ile	Arg	Ile	Ser	Asp	Arg	Gly	Gly		275	280	285	
Gly	Ile	Ala	His	Lys	Asp	Leu	Asp	Arg	Val	Met	Asp	Tyr	His	Phe	Thr	290	295	300	
Thr	Ala	Glu	Ala	Ser	Thr	Gln	Asp	Pro	Arg	Ile	Ser	Pro	Leu	Phe	Gly	305	310	315	320
His	Leu	Asp	Met	His	Ser	Gly	Gly	Gln	Ser	Gly	Pro	Met	His	Gly	Phe	325	330	335	
Gly	Phe	Gly	Leu	Pro	Thr	Ser	Arg	Ala	Tyr	Ala	Glu	Tyr	Leu	Gly	Gly	340	345	350	
Ser	Leu	Gln	Leu	Gln	Ser	Leu	Gln	Gly	Ile	Gly	Thr	Asp	Val	Tyr	Leu	355	360	365	
Arg	Leu	Arg	His	Ile	Asp	Gly	Arg	Glu	Glu	Ser	Phe	Arg	Ile			370	375	380	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 1335856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Glu	Thr	Val	Ile	Ser	Ser	Asp	Ser	Ser	Pro	Ala	Val	Glu	Asn	Glu	1	5	10	15
His	Pro	Gln	Glu	Thr	Pro	Glu	Ser	Asn	Asn	Ser	Val	Tyr	Thr	Ser	Phe	20	25	30	
Met	Lys	Ser	His	Arg	Cys	Tyr	Asp	Leu	Ile	Pro	Thr	Ser	Ser	Lys	Leu	35	40	45	
Val	Val	Phe	Asp	Thr	Ser	Leu	Gln	Val	Lys	Lys	Ala	Phe	Phe	Ala	Leu	50	55	60	
Val	Thr	Asn	Gly	Val	Arg	Ala	Ala	Pro	Leu	Trp	Asp	Ser	Lys	Lys	Gln	65	70	75	80
Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Asn	Ile	Leu	His	85	90	95	
Arg	Tyr	Tyr	Lys	Ser	Ala	Leu	Val	Gln	Ile	Tyr	Glu	Leu	Glu	Glu	His	100	105	110	
Lys	Ile	Glu	Thr	Trp	Arg	Glu	Val	Tyr	Leu	Gln	Asp	Ser	Phe	Lys	Pro	115	120	125	
Leu	Val	Cys	Ile	Ser	Pro	Asn	Ala	Ser	Leu	Phe	Asp	Ala	Val	Ser	Ser	130	135	140	
Leu	Ile	Arg	Asn	Lys	Ile	His	Arg	Leu	Pro	Val	Ile	Asp	Pro	Glu	Ser	145	150	155	160
Gly	Asn	Thr	Leu	Tyr	Ile	Leu	Thr	His	Lys	Arg	Ile	Leu	Lys	Phe	Leu	165	170	175	
Lys	Leu	Phe	Ile	Thr	Glu	Phe	Pro	Lys	Pro	Glu	Phe	Met	Ser	Lys	Ser	180	185	190	
Leu	Glu	Glu	Leu	Gln	Ile	Gly	Thr	Tyr	Ala	Asn	Ile	Ala	Met	Val	Arg	195	200	205	
Thr	Thr	Thr	Pro	Val	Tyr	Val	Ala	Leu	Gly	Ile	Phe	Val	Gln	His	Arg	210	215	220	
Val	Ser	Ala	Leu	Pro	Val	Val	Asp	Glu	Lys	Gly	Arg	Val	Val	Asp	Ile	225	230	235	240
Tyr	Ser	Lys	Phe	Asp	Val	Ile	Asn	Leu	Ala	Ala	Glu	Lys	Thr	Tyr	Asn	245	250	255	
Asn	Leu	Asp	Val	Ser	Val	Thr	Lys	Ala	Leu	Gln	His	Arg	Ser	His	Tyr	260	265	270	
Phe	Glu	Gly	Val	Leu	Lys	Cys	Tyr	Leu	His	Glu	Thr	Leu	Glu	Thr	Ile	275	280	285	
Ile	Asn	Arg	Leu	Val	Glu	Ala	Glu	Val	His	Arg	Leu	Val	Val	Val	Asp	290	295	300	
Glu	Asn	Asp	Val	Val	Lys	Gly	Ile	Val	Ser	Leu	Ser	Asp	Ile	Leu	Gln	305	310	315	320
Ala	Leu	Val	Leu	Thr	Gly	Gly	Glu	Lys	Lys	Pro						325	330		